

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2001, 12:06:13 ; Search time 16.04 Seconds
(without alignments)
1491.198 Million cell updates/sec

Title: US-09-486-334-2

Perfect score: 1641

Sequence: 1 MATCIDTRCGRNTQDDSRF.....IPCLTMDQTSYLTWMSDYVI 314

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1641	100.0	314	2	S67482
2	1611	98.2	314	2	S71181
3	1215	74.0	391	2	S63192
4	1105	67.3	303	2	S68469
5	877	53.4	347	2	T09140
6	869	53.0	294	2	A57478
7	849.5	51.8	312	2	S71207
8	699	42.6	315	2	C81184
9	649.5	39.6	272	2	C81184
10	648.5	39.5	273	1	XFECSA
11	648.5	39.5	273	2	S29568
12	648.5	39.5	273	2	F86036
13	647.5	39.5	273	2	G82049
14	643	39.2	308	2	T08867
15	624.5	38.1	267	2	G64080
16	587.5	35.8	299	2	T04669
17	573.5	34.9	274	2	A84936
18	549.5	33.5	261	1	JC1293
19	472.5	28.8	270	2	T50058
20	442	26.9	225	1	E53402
21	424	25.8	217	1	B53402
22	422.5	25.7	227	2	T44913
23	420.5	25.6	249	1	S75606
24	409	24.9	251	2	T44279
25	405	24.7	229	2	H70660
26	395	24.1	229	2	F83663
27	392	23.9	258	2	A83169
28	389.5	23.7	199	2	E86856
29	388.5	23.7	212	2	C81347

30	369.5	22.5	269	1	D43706	serine O-acetyltra
31	365	22.2	171	1	B64671	serine O-acetyltra
32	359	21.9	171	2	B71845	o-serine acetyltra
33	338.5	20.6	220	2	G72349	serine acetyltrans
34	312	19.0	171	2	D84302	serine acetyltrans
35	287	17.5	319	2	S55322	srpH protein - syn
36	265	16.1	231	2	H83381	probable acetyl tr
37	217	13.2	162	2	A64972	probable acetyl tr
38	217	13.2	162	2	B85832	probable transfera
39	207	12.6	184	2	C82264	serine acetyltrans
40	179	10.9	236	2	A86660	acetyltransferease
41	177.5	10.8	143	2	G82264	serine acetyltrans
42	175	10.7	236	2	H72245	2,3,4,5-tetrandro
43	175	10.7	240	2	E83983	tetrahydrodipicoll
44	171	10.4	201	2	H85806	hypothetical prote
45	164.5	10.0	190	2	S07000	nodulation protein

ALIGNMENTS

RESULT 1

S67482

serine O-acetyltransferase (EC 2.3.1.30), cytosolic - Arabidopsis thaliana

N/Alternate names: serine acetyltransferase

C/Species: Arabidopsis thaliana (mouse-ear cross)

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 05-May-2000

C/Accession: S67482; S52150

R/Ruifet, M.L.; Lebun, M.; Droux, M.; Douce, R.

Eur. J. Biochem. 227, 500-509, 1995

A/Title: Subcellular distribution of serine acetyltransferase from Pisum sativum and

A/Reference number: S67482; MUID:95154333

A/Accession type: DNA

A/Residues: 1-314 <RUF>

A/Cross-references: EMBL:Z34888; MID:9608676; PIDN:CAA84371.1; PID:9608677

A/Note: the authors translated the codon ACC for residue 158 as Ile and ACA for resid

C/Suprafamily: serine acetyltransferase; serine acetyltransferase homology

C/Keywords: acyltransferase; coenzyme A; cysteine biosynthesis

F:123-283/Domain: serine acetyltransferase homology <SAT>

Query Match	Best Local Similarity	100.0%	Score 1641	DB 2	Length 314
Matches 314	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	1	MATCIDTRCGRNTQDDSRFCCINFRPGSVNRKIHHTQIEDDDVWIKMLEAKSDV	60		
DB	1	MATCIDTRCGRNTQDDSRFCCINFRPGSVNRKIHHTQIEDDDVWIKMLEAKSDV	60		
QY	61	KOEPLSYVYVASTSHRSLSALAHITSVKLSNUNLPSTLFEFTSVLEESPEIEST	120		
DB	61	KOEPLSYVYVASTSHRSLSALAHITSVKLSNUNLPSTLFEFTSVLEESPEIEST	120		
QY	121	KODLAVNERDPACISYVHCFGLGKFLACQAHRIHTLMKONRKIVALLIONRVSSFA	180		
DB	121	KODLAVNERDPACISYVHCFGLGKFLACQAHRIHTLMKONRKIVALLIONRVSSFA	180		
QY	181	VDIHGAKIGKIGILDHATGTVYIGETAVVGNVSIHRYVTLGGTGKSGDRHPRKIGGVL	240		
DB	181	VDIHGAKIGKIGILDHATGTVYIGETAVVGNVSIHRYVTLGGTGKSGDRHPRKIGGVL	240		
QY	241	IGAGSCIIIGNTTIGGAKIGSGSVVVKDVPARTAVGNPARIIGKENPKRKHDPICITM	300		
DB	241	IGAGSCIIIGNTTIGGAKIGSGSVVVKDVPARTAVGNPARIIGKENPKRKHDPICITM	300		
QY	301	DQTSYLTWMSDYVI 314			
DB	301	DQTSYLTWMSDYVI 314			
RESULT	2	S71181			

QY 288 NPRKHD-KIPCLTMDOTSYLTMSDYVI 314
 Db 285 KPTIHDECEGCEGMDHRSFISEMSDYII 312

RESULT 8

F84554

Probable serine O-acetyltransferase [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: F84554

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beutlo, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffatt, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Niernann, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: F84554

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-315 <STO>

A:Cross-references: GB:AE002093; NID:96598796; PIDN:AAF18673.1; GSPDB:GN00139

C:Genetics:

A:Gene: Atg917640

A:Map position: 2

Query Match 42.6%; Score 699; DB 2; Length 315;

Best Local Similarity 50.2%; Pred. No. 1.6e-50;

Matches 141; Conservative 50; Mismatches 76; Indels 14; Gaps 4;

QY 27 FRPFSVNRK-IHHTQIEDD-----DVMKMLEAKSGDVKOEPIISNYVYASITSHRS 79

Db 8 FESGFEVYAKGTHKSEFSDNLDRPDRIMDAIREAK--LEKEPIISFLYAGLIAHDC 65

QY 80 LESALAHILSVKLSNLDPSNTLFEFLISVLESPPIESTKODLIAYKERDPACISYVH 139

Db 66 LEOALGFVLANRLQNPFTLATOLLDFYGVMMHDKIQGISIRHDLQAFKDRDPACISYSS 125

QY 140 CFFGFFGACQAHRIAHILMKONRKIVALLQNRVSEFANDIHGAKIGIGILLHAT 199

Db 126 AIIHLKGYALQAYRVANHLKLMWEGKRLALALQSRISVEFGIDHPRANIGEGILLDHGT 185

QY 200 GVTIGETAVAGDNVSLIHGVTIGTGKSGDRHPRKIGDVLGACSCILGNTIGEGAKI 259

Db 186 GVTIGETAVIGKVSILHGVTLGGTGKGEKDRHPRKIGEBALLGACVTLIGNISIGAMV 245

QY 260 GSGSVYKVPARTTAVGNPARLIGKENPRKHXDKIPCLTM 300

Db 246 AAGSLVKDVPSPHSVYVAGNPALKIRVME-----EODPSIAM 281

RESULT 9

C81184

Probable serine O-acetyltransferase (EC 2.3.1.30) NMA0742 [imported] - Neisseria meningi

C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001

C:Accession: C81184; H81917

R:Reitelsh, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

Science 287, 1809-1815, 2000

A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.; V

A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A:Reference number: A81000; MUID:20175755

A:Accession: C81184

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-272 <TET>

A:Cross-references: GB:AE002412; GB:AE002098; NID:97225783; PIDN:AAF40988.1; PID:9722578

A:Experimental source: serogroup B, strain MC58

R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

Nature 404, 502-506, 2000

A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491

A:Reference number: A81775; MUID:20222556

A:Accession: H81917

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-272 <PAR>

A:Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB84026.1; PID:9737

A:Experimental source: serogroup A, strain Z2491

C:Genetics:

A:Gene: cyse; NMB0560; NMA0742

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: acyltransferase; coenzyme A

F:88-246/Domain: serine acetyltransferase homology <SAT>

Query Match 39.6%; Score 649.5; DB 2; Length 272;

Best Local Similarity 50.7%; Pred. No. 1.7e-46;

Matches 136; Conservative 39; Mismatches 86; Indels 7; Gaps 2;

QY 47 DWIKMLEAKSDVKOEPIISNYVYASITSHRSLESAHLISVLSNLDPSNTLFEFL 106

Db 12 DLWHTIREETAAYASAEEMLASFLHQFVLRHESLSGLVLAHLSSKIGSPIMDVRALEIY 71

QY 107 ISVLESPPIESTKODLIAYKERDPACISYVHCFGKGFACQAHRIAHITMKONRKI 166

Db 72 QOALGSDTQICVADKALYERDPACDEYSPLLEFKGFHIAQHRIAHRIYLDGRK 131

QY 167 VALLIQRNVSSEFANDIHGAKIGIGILLDHATGVIGETAVAGDNVSLIHGVTIGTGK 226

Db 132 LAYFLQNNMSSEFVDHHPARFGYGLMDHATGCFVAGETAVAGDNVSLIHGVTIGTGK 191

QY 227 QSGDRHPRKIGDVLGACSCILGNTIGEGAKIGSGSVYKVPARTTAVGNPARLIGK 286

Db 192 EGDHRHPRKIGDVGAMGANSILGINRIGSNKAGAGSVVSDVPSITVGVPAKPAV-- 249

QY 287 ENPRKHKIPCLTMDOTSYLTMSDYVI 314

Db 250 ----RSLKTPSADMDQNIQTE-IDFWI 272

RESULT 10

XYESCA

serine O-acetyltransferase (EC 2.3.1.30) - Escherichia coli

C:Species: Escherichia coli

C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 05-May-2000

C:Accession: A27896; A34563; S47828; A65161

R:Denk, D.; Bock, A.

J. Gen. Microbiol. 133, 515-525, 1987

A:Title: L-Cysteine biosynthesis in Escherichia coli: nucleotide sequence and express

A:Reference number: A27896; MUID:88009872

A:Accession: A27896

A:Molecule type: DNA

A:Residues: 1-273 <DEN>

A:Cross-references: GB:M15745; NID:9145675; PIDN:AAA23648.1; PID:9145676

A:Experimental source: GB:M15745; NID:9145675; PIDN:AAA23648.1; PID:9145676

A:Title: Structure and expression of *cysX*, the second gene in the *Escherichia coli* K-

A:Accession: A34563

A:Molecule type: DNA

A:Residues: 1-273 <TEI>

A:Cross-references: GB:M34333; NID:9145693; PIDN:AAA23659.1; PID:9145694

A:Experimental source: GB:M34333; NID:9145693; PIDN:AAA23659.1; PID:9145694

A:Title: Submitted to the EMBL Data Library, March 1994

A:Reference number: S47828

A:Accession: S47828

A:Molecule type: DNA

A:Residues: 1-273 <PIU>

A:Cross-references: EMBL:U00039; NID:9466582; PIDN:AA18584.1; PID:9466745

A:Experimental source: EMBL:U00039; NID:9466582; PIDN:AA18584.1; PID:9466745

A:Title: R.F.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

A:Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of *Escherichia coli* K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: A65161

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-273 <BLAT>

A:Cross-references: GB:AE000438; GB:U00096; NID:q2367251; PIDN:MAC76631.1; PID:91790035;

A:Experimental source: strain K-12, substrain MG1655

C:Comment: This enzyme catalyzes the conversion of L-serine to O-acetyl serine (by acetyltransferase)

C:Gene: *cysE*

A:Map position: 81 min

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: aminoacyltransferase; coenzyme A; cysteine biosynthesis

F:84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 1; Length 273;

Best Local Similarity 50.8%; Pred. No. 2e-46;

Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

QY 43 EDDDDVWIKMEAKSDVQEPILSNYYASITSHRSLSALAHILSVKLSNLMPSNTL 102
 Db 4 EELEIWNKIKAKARTLADCEPMILASFYHATLLKHENLSALSYMLANKLSSPIMPALAI 63

QY 103 FELFISVLESPELIESRKODLIANKERDPACISYVHCFLEKFGFLACQAHRIATLTKQ 162
 Db 64 REVEEAYAADPEMISACDIAVTRDPADVKTSTPLLYLKGFHALQAYRIGHMLMQ 123

QY 163 NKRIVALIIONRVSESPAVDHPGAKIGKILLDHATGVIGETAVGVNDVSTLHGVTIG 222
 Db 124 GRRALATFLQNOVSVTFQVDIHPAKIGRIMLDHATGIYGETAVIENDVSTLQSVTLG 183

QY 223 GTGKSGDRHPKIGDGVILGAGSCILGNTTIGEGAKIGSGSVVKKVDPARTAVGNPARL 282
 Db 184 GTGKSGDRHPKIREGVIMGAKILGNIEVGRGAKIGAGSVVLQVPVPHHTAAGVPARI 243

QY 283 IGGKENPRKHKIPCLTMDQ 302
 Db 244 VGKPDSD---DK-PSMDMDQ 258

RESULT 11

S29368 serine O-acetyltransferase (EC 2.3.1.30) - *Salmonella typhimurium*

C:Species: *Salmonella typhimurium*

C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000

C:Accession: S29368

R:Submitted to: Kuczek, E.S.; Bawden, C.S.; Rogers, G.E.

A:Description: A novel biosynthetic pathway for mammalian cells by stable integration of

A:Reference number: S29567

A:Accession: S29568

A:Molecule type: DNA

A:Residues: 1-273 <SAT>

A:Cross-references: EMBL:X59594; NID:q47659; PIDN:CAA42163.1; PID:947660

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

C:Keywords: acyltransferase; coenzyme A

F:84-244/Domain: serine acetyltransferase homology <SAT>

Query Match 39.5%; Score 648.5; DB 2; Length 273;

Best Local Similarity 51.2%; Pred. No. 2e-46;

Matches 133; Conservative 50; Mismatches 72; Indels 5; Gaps 2;

QY 43 EDDDDVWIKMEAKSDVQEPILSNYYASITSHRSLSALAHILSVKLSNLMPSNTL 102
 Db 4 EELEIWNKIKAKARTLADCEPMILASFYHATLLKHENLSALSYMLANKLSSPIMPALAI 63

QY 103 FELFISVLESPELIESRKODLIANKERDPACISYVHCFLEKFGFLACQAHRIATLTKQ 162
 Db 64 REVEEAYAADPEMISACDIAVTRDPADVKTSTPLLYLKGFHALQAYRIGHMLMQ 123

QY 163 NKRIVALIIONRVSESPAVDHPGAKIGKILLDHATGVIGETAVGVNDVSTLHGVTIG 222

Db 124 GRRALATFLQNOVSVTFQVDIHPAKIGRIMLDHATGIYGETAVIENDVSTLQSVTLG 183

QY 223 GTGKSGDRHPKIGDGVILGAGSCILGNTTIGEGAKIGSGSVVKKVDPARTAVGNPARL 282

Db 184 GTGKSGDRHPKIREGVIMGAKILGNIEVGRGAKIGAGSVVLQVPVPHHTAAGVPARI 243

QY 283 IGGKENPRKHKIPCLTMDQ 302

Db 244 VGKPDSD---DK-PSMDMDQ 258

RESULT 12

serine acetyltransferase [imported] - *Escherichia coli* (strain O157:H7)

C:Species: *Escherichia coli*

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Mar-2001

C:Accession: F66036

P:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May

hiller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimantanta, E.; Potamouisis, K.; Apoda

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: F66036

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-273 <STO>

A:Cross-references: GB:AE005174; NID:q12518357; PIDN:AAG58754.1; GSPDB:GN00145; UMGF:

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: *cysE*

C:Superfamily: serine acetyltransferase; serine acetyltransferase homology

Query Match 39.5%; Score 648.5; DB 2; Length 273;

Best Local Similarity 50.8%; Pred. No. 2e-46;

Matches 132; Conservative 51; Mismatches 72; Indels 5; Gaps 2;

QY 43 EDDDDVWIKMEAKSDVQEPILSNYYASITSHRSLSALAHILSVKLSNLMPSNTL 102
 Db 4 EELEIWNKIKAKARTLADCEPMILASFYHATLLKHENLSALSYMLANKLSSPIMPALAI 63

QY 103 FELFISVLESPELIESRKODLIANKERDPACISYVHCFLEKFGFLACQAHRIATLTKQ 162
 Db 64 REVEEAYAADPEMISACDIAVTRDPADVKTSTPLLYLKGFHALQAYRIGHMLMQ 123

QY 163 NKRIVALIIONRVSESPAVDHPGAKIGKILLDHATGVIGETAVGVNDVSTLHGVTIG 222
 Db 124 GRRALATFLQNOVSVTFQVDIHPAKIGRIMLDHATGIYGETAVIENDVSTLQSVTLG 183

QY 223 GTGKSGDRHPKIGDGVILGAGSCILGNTTIGEGAKIGSGSVVKKVDPARTAVGNPARL 282
 Db 184 GTGKSGDRHPKIREGVIMGAKILGNIEVGRGAKIGAGSVVLQVPVPHHTAAGVPARI 243

QY 283 IGGKENPRKHKIPCLTMDQ 302
 Db 244 VGKPDSD---DK-PSMDMDQ 258

RESULT 13

S29049 serine acetyltransferase VC2649 [imported] - *Vibrio cholerae* (strain N16961 serogroup

C:Species: *Vibrio cholerae*

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: G82049

R:Heideberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gilm, M.L.; Dodson, R.

charlson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833

A:Accession: G82049
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1273 <HEI>
A:Cross-references: GB:AE004331; GB:AE003852; NID:g9657236; PIDN:AAF95790.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype EI Tor
C:Genetics:
A:Gene: VC2649
A:Map position: 1
C:Superfamily: serine acetyltransferase; serine acetyltransferase homology